Association of a lymphotoxin α gene polymorphism and atopy in Italian families

Elisabetta Trabetti, Cristina Patuzzo, Giovanni Malerba, Roberta Galavotti, Laura Carmen Martinati, Attilio L Boner, Pier Franco Pignatti

Abstract

Tumour necrosis factor (TNF) is a pro-inflammatory cytokine that increases human airway tissue responsiveness and is considered a candidate gene for asthma. Two common polymorphisms (LTαNcoI and TNFα-308) in the TNF gene complex were studied in 600 subjects from 131 Italian families with atopic asthmatic children. Skin prick test (SPT), total IgE levels, atopy (defined as increased IgE levels or SPT positivity or both), bronchial hyperresponsiveness, and clinical asthma were investigated. The observed distribution of the identical by descent allels at the LTαNcoI locus was different from expected for SPT and atopy (p=0.015). The LTαNcoI genotype distribution for increased IgE levels was different between males and females (p=0.0011), and an association of the 2.2 genotype with increased IgE levels was observed in females (p=0.0032). The results indicate that the LTα gene, or a closely linked locus, is associated with atopy, and suggest a sex difference in the effect of the gene.

Keywords: atopy; asthma; TNF; LTα

Asthma is an inflammatory disease of the lung that results in obstruction of the airways, characterised by airways hyperresponsiveness to various environmental stimuli.1 Most people with clinical asthma have evidence of increased bronchial responsiveness to methacholine (BHR).2 The majority of asthmatic children are also atopic, usually with raised total and allergen specific IgE or skin prick test reactivity or both. The aetiology of the disease is multifactorial, with environmental and hereditary determinants. Patterns of clustering and segregation analyses in asthma families have suggested a genetic component.4,5 Previous studies have found linkage of asthma and atopy to different candidate genes, among them tumour necrosis factor (TNF) and lymphotoxin α (LTα). TNF is a powerful proinflammatory cytokine that increases human airways responsiveness.6,7 LTα may regulate TNF gene expression.11 LTα and TNFα genes are located on chromosome 6 (6p21.1-6p21.3), between class II/III and class I clusters of the human major histocompatibility complex (MHC).12 Two polymorphisms of these genes have been described, the LTαNcoI polymorphism, located in the first intron,13 and the TNF-308 polymorphism, located in the promoter.14 Recently, these two polymorphisms have been associated with an increased risk of clinical asthma/BHR in two studies in the Australian population.15,16

The aim of the present study was to determine the involvement of the TNF genes in the genetic determination of asthma and allergy in a large series of Italian families.

Materials and methods

PATIENTS AND PHENOTYPES

A panel of 600 subjects belonging to 131 families from the Veneto region in north east Italy was recruited from atopic asthmatic children attending the Allergy and Pulmonology Clinic of the Department of Paediatrics of the University of Verona, as described before.16,17 All the subjects were tested for clinical history, total serum IgE level, skin prick test (SPT), and BHR. Clinical asthma was defined according to the American Thoracic Society criteria, including the response to a respiratory questionnaire. Atopy was defined by the presence of one or both of the following criteria: (1) positive SPT to one or more common aeroallergens (house dust mites, cat, dog, Alternaria grass pollen, Parietaria), or (2) raised circulating total IgE (from 0 to 10 years of age: age adjusted standard curve, levels above the 90th centile; above 10 years of age: >200 kU/l). Bronchial hyperreactivity to methacholine was defined as PC20<25 mg/ml.

The total number of patients was 397, of whom 367 were atopic, 329 positive for SPT, 236 with increased IgE levels, 221 with clinical asthma, and 232 with BHR. Seventy subjects with no clinical asthma, negative on SPT and BHR testing, and with known total serum IgE levels were used for LTαNcoI polymorphism case/control genotype frequency comparisons.

GENOTYPE ANALYSIS

Genomic DNA was extracted from whole blood by standard methods. LTα and TNFα polymorphisms were detected after PCR by restriction digestion of the products. For the LTαNcoI polymorphism we used the primers previously described,11 which generate a PCR product of 740 bp in size (LTαNcoI*2). Restriction of this product with NcoI results in fragments of 545 and 195 bp (LTαNcoI*1). For the TNF-308 polymorphism amplification, we used the primers previously described, in which the sequence of one primer was modified to incorporate NcoI restriction site.16 Restriction of the 107 bp product (TNF-308*2) with NcoI results in fragments of 87 and 20 bp (TNF-308*1). Allele denominations for
Table 1  Sharing of LTuNcoI and/or TNF-308 IBD alleles in affected sib pairs

<table>
<thead>
<tr>
<th>Trait</th>
<th>Marker</th>
<th>Alleles shared</th>
<th>2</th>
<th>1</th>
<th>0</th>
<th>p value*</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SPT</td>
<td>LTuNcoI</td>
<td>18</td>
<td>56.5</td>
<td>12.5</td>
<td>0.015</td>
<td></td>
</tr>
<tr>
<td></td>
<td>LTuNcoI/TNF-308</td>
<td>18.5</td>
<td>60.5</td>
<td>13</td>
<td>0.0075</td>
<td></td>
</tr>
<tr>
<td>Atopy</td>
<td>LTuNcoI</td>
<td>22</td>
<td>63.5</td>
<td>14.5</td>
<td>0.015</td>
<td></td>
</tr>
<tr>
<td></td>
<td>TNF-308</td>
<td>11</td>
<td>36.5</td>
<td>9.5</td>
<td>0.0075</td>
<td></td>
</tr>
<tr>
<td></td>
<td>LTuNcoI/TNF-308</td>
<td>23.5</td>
<td>66.5</td>
<td>15</td>
<td>0.012</td>
<td></td>
</tr>
</tbody>
</table>

Allele counts were performed with the GAS program.

* Expected allele sharing: 2 alleles = 0.25, 1 allele = 0.50, 0 alleles = 0.25.

Table 2  IgE and LTuNcoI genotypes of the females (and frequency)

<table>
<thead>
<tr>
<th>Increased IgE</th>
<th>LTuNcoI genotypes</th>
<th>1.1</th>
<th>1.2</th>
<th>2.2</th>
<th>Total</th>
<th>p value*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yes</td>
<td>3 (0.03)</td>
<td>27 (0.31)</td>
<td>58 (0.66)</td>
<td>88</td>
<td></td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>11 (0.05)</td>
<td>98 (0.48)</td>
<td>94 (0.46)</td>
<td>203</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*p value was determined on χ² in 3 classes observed.

Statistical analysis

Affected sib pair analysis was performed with the GAS program (http://www.ebi.ac.uk/ biocat/Genetic_tools.html) or with the SIBPAL program as implemented in the SAGE package. A non-parametric simulation based identity by descent (SimIBD) statistic was performed. Associations were tested by the Extended Transmission Disequilibrium Test (ETDT).

Results

We studied 600 subjects belonging to 131 families from the Veneto region of Italy, ascertained through atopic asthmatic children, plus 70 other subjects. All subjects were typed for two TNF gene polymorphisms, LTuNcoI, located in the first intron of the LTu gene, and TNF-308, located in the promoter of the TNFα gene.

Allele frequencies in the Italian families used in this study were determined on founding family members (n=267), irrespective of phenotype. The allele frequencies of LTuNcoI*1 and 2 (number of alleles counted=534) were 0.27 and 0.728, respectively. The allele frequencies (number of alleles counted=368) of TNF-308*1 and 2 were 0.856 and 0.144, respectively.

Linkage analysis between LTuNcoI and TNF-308 alleles, or LTuNcoI/TNF-308 haplotypes, and asthma, atopy, SPT, IgE, and BHR was performed. As shown in table 1, we observed a distortion of expected sharing in affected sib pairs of the LTuNcoI alleles and SPT or atopy (p=0.015). We also observed a distortion of expected allele sharing in affected sib pairs of the LTuNcoI/TNF-308 haplotypes with SPT or atopy (p=0.0075 and p=0.012, respectively), as shown in table 1. Analysis with the SIBPAL program of the estimated proportion of marker alleles shared (not shown in table 1) indicated a significant association with atopy of the LTuNcoI polymorphism (p=0.047) and of LTuNcoI/TNF-308 haplotypes (p=0.029). Simulation analysis on 1000 replicates indicated no significant association of the two polymorphisms, or of the haplotypes, with the five phenotypes considered. Transmission disequilibrium analysis with the ETDT program did not indicate any allele preferentially associated with any of the phenotypes.

When genotypes for LTuNcoI or TNF-308 were examined in the entire sample, no significant association was found with asthma, atopy, IgE, SPT, or BHR, although the LTuNcoI genotype distribution for increased IgE levels was significantly different between affected males and females (p=0.0011, data not shown). Table 2 shows the distribution of genotypes in affected versus unaffected females for total IgE level increase. The total IgE level increase was more commonly present in females with genotype 2.2 compared to those with genotypes 1.1 plus 1.2 (p=0.0032, OR=2.24, 1.29-3.90). No significant association of the LTuNcoI genotypes in affected males (n=338) was observed.

Discussion

The results obtained on atopic asthmatic subjects by the analysis of polymorphisms for the two TNF loci show a significant allele sharing for the LTuNcoI polymorphism and atopy, but not for the BHR phenotype or for clinical asthma. The LTuNcoI*2 allele is associated with a lower LTα response15 and a higher TNFα level.16 It is possible that the LTα gene intron 1, which contains the NcoI polymorphism, includes a regulatory element which may affect TNFα gene expression.17

Two papers on the south western Australian population reported similar investigations. One analysis was performed on 413 subjects in 88 families from a general population sample from Busselton,18 another was a case-control study on 74 asthmatic and 50 non-asthmatic children from Perth.19 The population allele frequency distribution at the two loci was significantly different in the three asthmatic population samples. LTuNcoI*2 was 0.72, 0.55, or 0.65, in the Italian, in the Busselton, and in the Perth populations, respectively. TNF-308*1 was 0.84, 0.70, or 0.83, in the Italian, in the Busselton, and in the Perth populations, respectively. In the Busselton study,18 genotypes LTuNcoI 1.1, TNF-308 2.2, and haplotypes LTuNcoI*1/TNF-308*2 were all signifi-
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